0590
0730   #8

```
RAW SEQUENCE LISTING              DATE: 08/02/2002
PATENT APPLICATION:  US/09/989,981A   TIME: 08:55:39

Input Set : A:\-73-2.app
Output Set: N:\CRF3\08022002\I989981A.raw
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```
 3 <110> APPLICANT: Hobbs, Helen H.
 4        Shan, Bei
 5        Barnes, Robert
 6        Tian, Hui
 7        Tularik Inc.
 8        Board of Regents, The University of Texas System
10 <120> TITLE OF INVENTION: ABCG5 and ABCG8: Compositions and Methods of Use
12 <130> FILE REFERENCE: 018781-007320US
14 <140> CURRENT APPLICATION NUMBER: US 09/989,981A
15 <141> CURRENT FILING DATE: 2002-07-23
17 <150> PRIOR APPLICATION NUMBER: US 60/252,235
18 <151> PRIOR FILING DATE: 2000-11-20
20 <150> PRIOR APPLICATION NUMBER: US 60/253,645
21 <151> PRIOR FILING DATE: 2000-11-28
23 <160> NUMBER OF SEQ ID NOS: 13
25 <170> SOFTWARE: PatentIn Ver. 2.1
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 1959
29 <212> TYPE: DNA
30 <213> ORGANISM: Mus musculus
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (1)..(1959)
35 <223> OTHER INFORMATION: mouse ABCG5 (mABCG5)
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40  1               5                  10                  15
42 atc aac aga ggg tct ctg agc tcc ctg gag caa ggt tcg gtc acg ggc    96
43 Ile Asn Arg Gly Ser Leu Ser Ser Leu Glu Gln Gly Ser Val Thr Gly
44              20                  25                  30
46 aca gag gct cgg cac agc tta ggt gtc ctg cat gtg tcc tac agc gtc   144
47 Thr Glu Ala Arg His Ser Leu Gly Val Leu His Val Ser Tyr Ser Val
48          35                  40                  45
50 agc aac cgt gtc ggg cct tgg tgg aac atc aaa tca tgc cag cag aag   192
51 Ser Asn Arg Val Gly Pro Trp Trp Asn Ile Lys Ser Cys Gln Gln Lys
52      50                  55                  60
54 tgg gac agg caa atc ctc aaa gat gtc tcc ttg tac atc gag agt ggc   240
55 Trp Asp Arg Gln Ile Leu Lys Asp Val Ser Leu Tyr Ile Glu Ser Gly
56  65                  70                  75                  80
58 cag att atg tgc atc tta ggc agc tca ggc tca ggg aag acc acg ctg   288
59 Gln Ile Met Cys Ile Leu Gly Ser Ser Gly Ser Gly Lys Thr Thr Leu
60              85                  90                  95
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62 ctg gac gcc atc tcc ggg agg ctg cgg cgc act ggg acc ctg gaa ggg    336
63 Leu Asp Ala Ile Ser Gly Arg Leu Arg Arg Thr Gly Thr Leu Glu Gly
64             100             105             110
66 gag gtg ttt gtg aat ggc tgc gag ctg cgc agg gac cag ttc caa gac    384
67 Glu Val Phe Val Asn Gly Cys Glu Leu Arg Arg Asp Gln Phe Gln Asp
68             115             120             125
70 tgc ttc tcc tac gtc ctg cag agc gac gtt ttt ctg agc agc ctc act    432
71 Cys Phe Ser Tyr Val Leu Gln Ser Asp Val Phe Leu Ser Ser Leu Thr
72     130             135             140
74 gtg cgc gag acg ttg cga tac aca gcg atg ctg gcc ctc tgc cgc agc    480
75 Val Arg Glu Thr Leu Arg Tyr Thr Ala Met Leu Ala Leu Cys Arg Ser
76 145             150          ·      155             160
78 tcc gcg gac ttc tac aac aag aag gta gag gca gtc atg aca gag ctg    528
79 Ser Ala Asp Phe Tyr Asn Lys Lys Val Glu Ala Val Met Thr Glu Leu
80             165             170             175
82 agc ctg agc cac gtg gcg gac caa atg att ggc agc tat aat ttt ggg    576
83 Ser Leu Ser His Val Ala Asp Gln Met Ile Gly Ser Tyr Asn Phe Gly
84             180             185             190
86 gga att tcc agt ggc gag cgg cgc cga gtt tcc atc gca gcc caa ctc    624
87 Gly Ile Ser Ser Gly Glu Arg Arg Arg Val Ser Ile Ala Ala Gln Leu
88             195             200             205
90 ctt cag gac ccc aag gtc atg atg cta gat gag cca acc aca gga ctg    672
91 Leu Gln Asp Pro Lys Val Met Met Leu Asp Glu Pro Thr Thr Gly Leu
92     210             215             220
94 gac tgc atg act gca aat caa att gtc ctt ctc ttg gct gag ctg gct    720
95 Asp Cys Met Thr Ala Asn Gln Ile Val Leu Leu Leu Ala Glu Leu Ala
96 225             230             235             240
98 cgc agg gac cga att gtg att gtc acc atc cac cag cct cgc tct gag    768
99 Arg Arg Asp Arg Ile Val Ile Val Thr Ile His Gln Pro Arg Ser Glu
100            245             250             255
102 ctc ttc caa cac ttc gac aaa att gcc atc ctg act tac gga gag ttg   816
103 Leu Phe Gln His Phe Asp Lys Ile Ala Ile Leu Thr Tyr Gly Glu Leu
104            260             265             270
106 gtg ttc tgt ggc acc cca gag gag atg ctt ggc ttc ttc aat aac tgt   864
107 Val Phe Cys Gly Thr Pro Glu Glu Met Leu Gly Phe Phe Asn Asn Cys
108            275             280             285
110 ggt tac ccc tgt cct gaa cat tcc aat ccc ttt gat ttt tac atg gac   912
111 Gly Tyr Pro Cys Pro Glu His Ser Asn Pro Phe Asp Phe Tyr Met Asp
112     290             295             300
114 ttg aca tca gtg gac acc caa agc aga gag cgg gaa ata gaa acg tac   960
115 Leu Thr Ser Val Asp Thr Gln Ser Arg Glu Arg Glu Ile Glu Thr Tyr
116 305             310             315             320
118 aag cga gta cag atg ctg gaa tgt gcc ttc aag gaa tct gac atc tat  1008
119 Lys Arg Val Gln Met Leu Glu Cys Ala Phe Lys Glu Ser Asp Ile Tyr
120             325             330             335
122 cac aaa att ctg gag aac att gaa aga gca cga tac ctg aaa acc tta  1056
123 His Lys Ile Leu Glu Asn Ile Glu Arg Ala Arg Tyr Leu Lys Thr Leu
124             340             345             350
126 ccc atg gtt cct ttc aaa aca aaa gat cct cct ggg atg ttc ggc aag  1104
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127 Pro Met Val Pro Phe Lys Thr Lys Asp Pro Pro Gly Met Phe Gly Lys
128         355             360             365
130 ctt ggt gtc ctg ctg agg cga gta aca aga aac tta atg agg aat aag    1152
131 Leu Gly Val Leu Leu Arg Arg Val Thr Arg Asn Leu Met Arg Asn Lys
132         370             375             380
134 cag gca gtg att atg cgt ctc gtt cag aat ctg atc atg ggc ctc ttc    1200
135 Gln Ala Val Ile Met Arg Leu Val Gln Asn Leu Ile Met Gly Leu Phe
136 385             390             395             400
138 ctc att ttc tac ctt ctc cgc gtc cag aac aac acg cta aag ggc gct    1248
139 Leu Ile Phe Tyr Leu Leu Arg Val Gln Asn Asn Thr Leu Lys Gly Ala
140         405             410             415
142 gtg cag gac cgc gtg ggg ctg ctc tat cag ctt gtg ggt gcc acc cca    1296
143 Val Gln Asp Arg Val Gly Leu Leu Tyr Gln Leu Val Gly Ala Thr Pro
144         420             425             430
146 tac acc ggc atg ctc aat gct gtg aat ctg ttt ccc atg ctg aga gcc    1344
147 Tyr Thr Gly Met Leu Asn Ala Val Asn Leu Phe Pro Met Leu Arg Ala
148         435             440             445
150 gtc agc gac cag gag agt cag gat ggc ctg tat cat aag tgg cag atg    1392
151 Val Ser Asp Gln Glu Ser Gln Asp Gly Leu Tyr His Lys Trp Gln Met
152         450             455             460
154 ctg ctc gcc tac gtg cta cac gtc ctc ccc ttc agc gtc atc gcc acg    1440
155 Leu Leu Ala Tyr Val Leu His Val Leu Pro Phe Ser Val Ile Ala Thr
156 465             470             475             480
158 gtc att ttc agc agt gtg tgt tat tgg act ctg ggc ttg tat cct gaa    1488
159 Val Ile Phe Ser Ser Val Cys Tyr Trp Thr Leu Gly Leu Tyr Pro Glu
160         485             490             495
162 gtt gcc aga ttt gga tat ttc tct gct gct ctt ttg gcc cct cac tta    1536
163 Val Ala Arg Phe Gly Tyr Phe Ser Ala Ala Leu Leu Ala Pro His Leu
164         500             505             510
166 att gga gaa ttt cta aca ctt gtg ctg ctt ggt ata gtc caa aac cct    1584
167 Ile Gly Glu Phe Leu Thr Leu Val Leu Leu Gly Ile Val Gln Asn Pro
168         515             520             525
170 aat att gtc aac agt ata gtg gct ctg ctc agc atc tct ggg ctg ctt    1632
171 Asn Ile Val Asn Ser Ile Val Ala Leu Leu Ser Ile Ser Gly Leu Leu
172         530             535             540
174 att gga tct gga ttt atc aga aac ata caa gaa atg ccc att cct tta    1680
175 Ile Gly Ser Gly Phe Ile Arg Asn Ile Gln Glu Met Pro Ile Pro Leu
176 545             550             555             560
178 aaa atc ctg ggt tat ttt aca ttc caa aaa tac tgt tgt gag att ctc    1728
179 Lys Ile Leu Gly Tyr Phe Thr Phe Gln Lys Tyr Cys Cys Glu Ile Leu
180         565             570             575
182 gtg gtc aat gag ttt tac ggc ctg aac ttc act tgt ggt gga tcc aac    1776
183 Val Val Asn Glu Phe Tyr Gly Leu Asn Phe Thr Cys Gly Gly Ser Asn
184         580             585             590
186 acc tct atg cta aat cac ccg atg tgc gcc atc acc caa ggg gtc cag    1824
187 Thr Ser Met Leu Asn His Pro Met Cys Ala Ile Thr Gln Gly Val Gln
188         595             600             605
190 ttc atc gag aaa acc tgc cca ggt gct aca tcc aga ttc acg gca aac    1872
191 Phe Ile Glu Lys Thr Cys Pro Gly Ala Thr Ser Arg Phe Thr Ala Asn
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PATENT APPLICATION: US/09/989,981A   TIME: 08:55:39

          Input Set : A:\-73-2.app
          Output Set: N:\CRF3\08022002\I989981A.raw

192   610   615   620
194 ttc ctc atc tta tat ggg ttt atc cca gct ctg gtc atc cta gga ata   1920
195 Phe Leu Ile Leu Tyr Gly Phe Ile Pro Ala Leu Val Ile Leu Gly Ile
196 625   630   635   640
198 gtg att ttt aaa gtc agg gac tac ctg att agc aga tag   1959
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200   645   650
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204 <211> LENGTH: 652
205 <212> TYPE: PRT
206 <213> ORGANISM: Mus musculus
208 <220> FEATURE:
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215   20   25   30
216 Thr Glu Ala Arg His Ser Leu Gly Val Leu His Val Ser Tyr Ser Val
217   35   40   45
218 Ser Asn Arg Val Gly Pro Trp Trp Asn Ile Lys Ser Cys Gln Gln Lys
219   50   55   60
220 Trp Asp Arg Gln Ile Leu Lys Asp Val Ser Leu Tyr Ile Glu Ser Gly
221 65   70   75   80
222 Gln Ile Met Cys Ile Leu Gly Ser Ser Gly Ser Gly Lys Thr Thr Leu
223   85   90   95
224 Leu Asp Ala Ile Ser Gly Arg Leu Arg Arg Thr Gly Thr Leu Glu Gly
225   100   105   110
226 Glu Val Phe Val Asn Gly Cys Glu Leu Arg Arg Asp Gln Phe Gln Asp
227   115   120   125
228 Cys Phe Ser Tyr Val Leu Gln Ser Asp Val Phe Leu Ser Ser Leu Thr
229   130   135   140
230 Val Arg Glu Thr Leu Arg Tyr Thr Ala Met Leu Ala Leu Cys Arg Ser
231 145   150   155   160
232 Ser Ala Asp Phe Tyr Asn Lys Lys Val Glu Ala Val Met Thr Glu Leu
233   165   170   175
234 Ser Leu Ser His Val Ala Asp Gln Met Ile Gly Ser Tyr Asn Phe Gly
235   180   185   190
236 Gly Ile Ser Ser Gly Glu Arg Arg Arg Val Ser Ile Ala Ala Gln Leu
237   195   200   205
238 Leu Gln Asp Pro Lys Val Met Met Leu Asp Glu Pro Thr Thr Gly Leu
239   210   215   220
240 Asp Cys Met Thr Ala Asn Gln Ile Val Leu Leu Leu Ala Glu Leu Ala
241 225   230   235   240
242 Arg Arg Asp Arg Ile Val Ile Val Thr Ile His Gln Pro Arg Ser Glu
243   245   250   255
244 Leu Phe Gln His Phe Asp Lys Ile Ala Ile Leu Thr Tyr Gly Glu Leu
245   260   265   270
246 Val Phe Cys Gly Thr Pro Glu Glu Met Leu Gly Phe Phe Asn Asn Cys

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247          275                    280            .     285
248 Gly Tyr Pro Cys Pro Glu His Ser Asn Pro Phe Asp Phe Tyr Met Asp
249     290                    295                300
250 Leu Thr Ser Val Asp Thr Gln Ser Arg Glu Arg Glu Ile Glu Thr Tyr
251 305                    310                315                320
252 Lys Arg Val Gln Met Leu Glu Cys Ala Phe Lys Glu Ser Asp Ile Tyr
253                 325                330                335
254 His Lys Ile Leu Glu Asn Ile Glu Arg Ala Arg Tyr Leu Lys Thr Leu
255                 340                345                350
256 Pro Met Val Pro Phe Lys Thr Lys Asp Pro Pro Gly Met Phe Gly Lys
257         355                360                365
258 Leu Gly Val Leu Leu Arg Arg Val Thr Arg Asn Leu Met Arg Asn Lys
259     370                375                .380
260 Gln Ala Val Ile Met Arg Leu Val Gln Asn Leu Ile Met Gly Leu Phe
261 385                    390                395                400
262 Leu Ile Phe Tyr Leu Leu Arg Val Gln Asn Asn Thr Leu Lys Gly Ala
263                 405                410                415
264 Val Gln Asp Arg Val Gly Leu Leu Tyr Gln Leu Val Gly Ala Thr Pro
265                 420          .     425                430
266 Tyr Thr Gly Met Leu Asn Ala Val Asn Leu Phe Pro Met Leu Arg Ala
267         435                440                445
268 Val Ser Asp Gln Glu Ser Gln Asp Gly Leu Tyr His Lys Trp Gln Met
269     450                455              .   460
270 Leu Leu Ala Tyr Val Leu His Val Leu Pro Phe Ser Val Ile Ala Thr
271 465                    470                475                480
272 Val Ile Phe Ser Ser Val Cys Tyr Trp Thr Leu Gly Leu Tyr Pro Glu
273                 485                490                495
274 Val Ala Arg Phe Gly Tyr Phe Ser Ala Ala Leu Leu Ala Pro His Leu
275             500                505                510   .
276 Ile Gly Glu Phe Leu Thr Leu Val Leu Leu Gly Ile Val Gln Asn Pro
277         515                520                525
278 Asn Ile Val Asn Ser Ile Val Ala Leu Leu Ser Ile Ser Gly Leu Leu
279     530                535                540
280 Ile Gly Ser Gly Phe Ile Arg Asn Ile Gln Glu Met Pro Ile Pro Leu
281 545                    550                555                560
282 Lys Ile Leu Gly Tyr Phe Thr Phe Gln Lys Tyr Cys Cys Glu Ile Leu
283             565                570                575
284 Val Val Asn Glu Phe Tyr Gly Leu Asn Phe Thr Cys Gly Gly Ser Asn
285             580                585                590
286 Thr Ser Met Leu Asn His Pro Met Cys Ala Ile Thr Gln Gly Val Gln
287         595                600               .     605
288 Phe Ile Glu Lys Thr Cys Pro Gly Ala Thr Ser Arg Phe Thr Ala Asn
289     610                ,615                620
290 Phe Leu Ile Leu Tyr Gly Phe Ile Pro Ala Leu Val Ile Leu Gly Ile
291 625                    630                635                640
292 Val Ile Phe Lys Val Arg Asp Tyr Leu Ile Ser Arg
293             645                650
296 <210> SEQ ID NO: 3
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VERIFICATION SUMMARY   DATE: 08/02/2002
PATENT APPLICATION: **US/09/989,981A**   TIME: 08:55:40

Input Set : **A:\-73-2.app**
Output Set: **N:\CRF3\08022002\I989981A.raw**

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date